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Abstract of the Disclosure

The invention relates to a method of typing a sample of nucleic acid molecules in DNA sequencing technologies, whereby the molecules are suspected to comprise at least DNA from one type or species, e.g. microorganisms or viruses, with each species or type or target DNA having different nucleotide patterns. By adding a mixed set of at least two oligonucleotide primers, whereby each primer is designed for being specific for one type or species or target DNA, thereby allowing a primer or primers to hybridize in or close to the type-specific or target regions; determining the types or targets sequence by extending the hybridized primer or primers in a sequencing reaction. Hereby, the typing is simplified by using a set of type-specific primers and sequence pattern recognition approach. The method of invention is suitable for samples containing a plurality of types or species, multiple pathogenic infections or variants, and amplicons with unspecific amplification products. Furthermore, the invention relates to a kit for use in the method.